



SEQUENCE LISTING

<110> Allison, Anthony

<120> MODIFIED ANNEXIN PROTEINS AND METHODS FOR TREATING VASO-OCCLUSIVE
SICKLE-CELL DISEASE

<130> SURR.113

<150> 60/400,718

<151> 2002-08-02

<150> 10/080,370

<151> 2002-02-21

<160> 9

<170> PatentIn version 3.2

<210> 1

<211> 957

<212> DNA

<213> Homo sapiens

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ttgacatccc gaagtaatgc tcagcgccag gaaatctctg cagcttttaa gactctgttt	180
ggcagggatc ttctggatga cctgaaatca gaactaactg gaaaatttga aaaattaatt	240
gtggctctga tgaaaccctc tcggctttat gatgcttatg aactgaaaca tgccttgaag	300
ggagctggaa caaatgaaaa agtactgaca gaaattattg cttcaaggac acctgaagaa	360
ctgagagcca tcaaacaagt ttatgaagaa gaatatggct caagcctgga agatgacgtg	420
gtgggggaca cttcagggtg ctaccagcgg atgttggttg ttctccttca ggctaacaga	480
gaccctgatg ctggaattga tgaagctcaa gttgaacaag atgctcaggc tttatttcag	540
gctggagaac ttaaatgggg gacagatgaa gaaaagttaa tcaccatctt tggaacacga	600
agtgtgtctc atttgagaaa ggtgtttgac aagtacatga ctatatcagg atttcaaatt	660
gaggaaacca ttgaccgca gacttctggc aatttagagc aactactcct tgctgttgtg	720
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gctgggacag atgatcatc cctcatcaga gtcattggtt ccaggagtga gattgatctg	840
tttaacatca ggaaggagt taggaagaat ttgcccacct ctctttattc catgattaag	900
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 1 5 10 15
 cgg gct gat gca gaa act ctt cgg aag gct atg aaa ggc ttg ggc aca 96
 Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys Gly Leu Gly Thr
 20 25 30
 gat gag gag agc atc ctg act ctg ttg aca tcc cga agt aat gct cag 144
 Asp Glu Glu Ser Ile Leu Thr Leu Leu Thr Ser Arg Ser Asn Ala Gln
 35 40 45
 cgc cag gaa atc tct gca gct ttt aag act ctg ttt ggc agg gat ctt 192
 Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr Leu Phe Gly Arg Asp Leu
 50 55 60
 ctg gat gac ctg aaa tca gaa cta act gga aaa ttt gaa aaa tta att 240
 Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile
 65 70 75 80
 gtg gct ctg atg aaa ccc tct cgg ctt tat gat gct tat gaa ctg aaa 288
 Val Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys
 85 90 95
 cat gcc ttg aag gga gct gga aca aat gaa aaa gta ctg aca gaa att 336
 His Ala Leu Lys Gly Ala Gly Thr Asn Glu Lys Val Leu Thr Glu Ile
 100 105 110
 att gct tca agg aca cct gaa gaa ctg aga gcc atc aaa caa gtt tat 384
 Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Val Tyr
 115 120 125
 gaa gaa gaa tat ggc tca agc ctg gaa gat gac gtg gtg ggg gac act 432
 Glu Glu Glu Tyr Gly Ser Ser Leu Glu Asp Asp Val Val Gly Asp Thr
 130 135 140
 tca ggg tac tac cag cgg atg ttg gtg gtt ctc ctt cag gct aac aga 480
 Ser Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg
 145 150 155 160
 gac cct gat gct gga att gat gaa gct caa gtt gaa caa gat gct cag 528
 Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln Val Glu Gln Asp Ala Gln
 165 170 175

gct tta ttt cag gct gga gaa ctt aaa tgg ggg aca gat gaa gaa aag	576
Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys	
180 185 190	
ttt atc acc atc ttt gga aca cga agt gtg tct cat ttg aga aag gtg	624
Phe Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Lys Val	
195 200 205	
ttt gac aag tac atg act ata tca gga ttt caa att gag gaa acc att	672
Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile	
210 215 220	
gac cgc gag act tct ggc aat tta gag caa cta ctc ctt gct gtt gtg	720
Asp Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Leu Ala Val Val	
225 230 235 240	
aaa tct att cga agt ata cct gcc tac ctt gca gag acc ctc tat tat	768
Lys Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr	
245 250 255	
gct atg aag gga gct ggg aca gat gat cat acc ctc atc aga gtc atg	816
Ala Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Met	
260 265 270	
gtt tcc agg agt gag att gat ctg ttt aac atc agg aag gag ttt agg	864
Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg	
275 280 285	
aag aat ttt gcc acc tct ctt tat tcc atg att aag gga gat aca tct	912
Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser	
290 295 300	
ggg gac tat aag aaa gct ctt ctg ctg ctc tgt gga gaa gat gac	957
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305 310 315	

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 <212> PRT
 <213> Homo sapiens

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35 40 45	

Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr Leu Phe Gly Arg Asp Leu
 50 55 60

Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile
 65 70 75 80

Val Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys
 85 90 95

His Ala Leu Lys Gly Ala Gly Thr Asn Glu Lys Val Leu Thr Glu Ile
 100 105 110

Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Val Tyr
 115 120 125

Glu Glu Glu Tyr Gly Ser Ser Leu Glu Asp Asp Val Val Gly Asp Thr
 130 135 140

Ser Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg
 145 150 155 160

Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln Val Glu Gln Asp Ala Gln
 165 170 175

Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys
 180 185 190

Phe Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Lys Val
 195 200 205

Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile
 210 215 220

Asp Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Leu Ala Val Val
 225 230 235 240

Lys Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr
 245 250 255

Ala Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Met
 260 265 270

Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg
 275 280 285

Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser
 290 295 300

Gly Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Glu Asp Asp
 305 310 315

<210> 4
 <211> 2016
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (1000)..(1002)
 <223> n = a, c, t, or g

<220>
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 <222> (1051)..(1053)
 <223> n = a, c, t, or g

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 aagggcctgg gcaccgacga ggactccatc ctgaacctgc tgaccgcccg ctccaacgcc 180
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 cgctgttacg acgcctacga gctgaagcac gccaaagctgg gcgccggcac cgacgagaag 360
 gtgctgaccg agatcatcgc ctcccgacc cccgaggagc tgcgcgccat caagcaggcc 420
 tacgaggagg agtacggctc caacctggag gacgacgtgg tgggcgacac ctccggctac 480
 taccagcgca tgctggtggt gctgctgcag gccaaaccgcg accccgacac cgccatcgac 540
 gacgcccagg tggagctgga cgcccaggcc ctgttccagg ccggcgagct gaagtggggc 600

accgacgagg agaagttcat caccatcctg ggcacccgct ccgtgtccca cctgcgccgc	660
gtgttcgaca agtacatgac catctccggc ttccagatcg aggagaccat cgaccgcgag	720
acctccggca acctggagaa cctgctgctg gccgtggtga agtccatccg ctccatcccc	780
gcctacctgg ccgagaccct gtactacgcc atgaagggcg ccggcaccga cgaccacacc	840
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cgcaagaact tcgccacctc cctgtactcc atgatcaagg gcgacacctc cggcgactac	960
aagaaggccc tgctgctgct gtgcggcggc gaggacgacn nnagatctcg atcgggcctg	1020
gaggtgctgt tccagggccc cggaagtact nnngccctgc gcggcaccgt gaccgacttc	1080
tccggcttcg acggccgcgc cgacgccgag gtgctgcgca aggccatgaa gggcctgggc	1140
accgacgagg actccatcct gaacctgctg accgcccgt ccaacgcccc gcgccagcag	1200
atcgccgagg agttcaagac cctgttcggc cgcgacctgg tgaacgacat gaagtccgag	1260
ctgaccggca agttcgagaa gctgatcgtg gccctgatga agccctcccg cctgtacgac	1320
gcctacgagc tgaagcacgc caagctgggc gccggcaccg acgagaaggt gctgaccgag	1380
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ctggtggtgc tgctgcaggc caaccgcgac cccgacaccg ccatcgacga cgcccagggtg	1560
gagctggacg cccaggccct gttccaggcc ggcgagctga agtggggcac cgacgaggag	1620
aagttcatca ccatcctggg caccgcctcc gtgtcccacc tgcgccgcgt gttcgacaag	1680
tacatgacca tctccggctt ccagatcgag gagaccatcg accgcgagac ctccggcaac	1740
ctggagaacc tgctgctggc cgtggtgaag tccatccgct ccatccccgc ctacctggcc	1800
gagaccctgt actacgccat gaagggcgcc ggcaccgacg accacaccct gatccgcgtg	1860
atcgtgtccc gctccgagat cgacctgttc aacatccgca aggagtccg caagaacttc	1920
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<210> 5
 <211> 2016
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

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tac cag cgc atg ctg gtg gtg ctg ctg cag gcc aac cgc gac ccc gac	528
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp	
165 170 175	
acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc ctg ttc	576
Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe	
180 185 190	
cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc atc acc	624
Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr	
195 200 205	
atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc gac aag	672
Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys	
210 215 220	
tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac cgc gag	720
Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu	
225 230 235 240	
acc tcc ggc aac ctg gag aac ctg ctg ctg gcc gtg gtg aag tcc atc	768
Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile	
245 250 255	
cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc atg aag	816
Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys	
260 265 270	
ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc	864
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg	
275 280 285	
tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc	912
Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe	
290 295 300	
gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac	960
Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr	
305 310 315 320	
aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac nnn aga tct	1008
Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser	
325 330 335	
cga tcg ggc ctg gag gtg ctg ttc cag ggc ccc gga agt act nnn gcc	1056
Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala	
340 345 350	
ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac	1104
Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp	
355 360 365	
gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac	1152

Ala	Glu	Val	Leu	Arg	Lys	Ala	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Asp		
370						375					380						
tcc	atc	ctg	aac	ctg	ctg	acc	gcc	cgc	tcc	aac	gcc	cag	cgc	cag	cag	1200	
Ser	Ile	Leu	Asn	Leu	Leu	Thr	Ala	Arg	Ser	Asn	Ala	Gln	Arg	Gln	Gln		
385					390					395					400		
atc	gcc	gag	gag	ttc	aag	acc	ctg	ttc	ggc	cgc	gac	ctg	gtg	aac	gac	1248	
Ile	Ala	Glu	Glu	Phe	Lys	Thr	Leu	Phe	Gly	Arg	Asp	Leu	Val	Asn	Asp		
				405					410					415			
atg	aag	tcc	gag	ctg	acc	ggc	aag	ttc	gag	aag	ctg	atc	gtg	gcc	ctg	1296	
Met	Lys	Ser	Glu	Leu	Thr	Gly	Lys	Phe	Glu	Lys	Leu	Ile	Val	Ala	Leu		
			420					425					430				
atg	aag	ccc	tcc	cgc	ctg	tac	gac	gcc	tac	gag	ctg	aag	cac	gcc	aag	1344	
Met	Lys	Pro	Ser	Arg	Leu	Tyr	Asp	Ala	Tyr	Glu	Leu	Lys	His	Ala	Lys		
		435					440					445					
ctg	ggc	gcc	ggc	acc	gac	gag	aag	gtg	ctg	acc	gag	atc	atc	gcc	tcc	1392	
Leu	Gly	Ala	Gly	Thr	Asp	Glu	Lys	Val	Leu	Thr	Glu	Ile	Ile	Ala	Ser		
	450					455					460						
cgc	acc	ccc	gag	gag	ctg	cgc	gcc	atc	aag	cag	gcc	tac	gag	gag	gag	1440	
Arg	Thr	Pro	Glu	Glu	Leu	Arg	Ala	Ile	Lys	Gln	Ala	Tyr	Glu	Glu	Glu		
465					470					475					480		
tac	ggc	tcc	aac	ctg	gag	gac	gac	gtg	gtg	ggc	gac	acc	tcc	ggc	tac	1488	
Tyr	Gly	Ser	Asn	Leu	Glu	Asp	Asp	Val	Val	Gly	Asp	Thr	Ser	Gly	Tyr		
			485						490					495			
tac	cag	cgc	atg	ctg	gtg	gtg	ctg	ctg	cag	gcc	aac	cgc	gac	ccc	gac	1536	
Tyr	Gln	Arg	Met	Leu	Val	Val	Leu	Leu	Gln	Ala	Asn	Arg	Asp	Pro	Asp		
			500					505					510				
acc	gcc	atc	gac	gac	gcc	cag	gtg	gag	ctg	gac	gcc	cag	gcc	ctg	ttc	1584	
Thr	Ala	Ile	Asp	Asp	Ala	Gln	Val	Glu	Leu	Asp	Ala	Gln	Ala	Leu	Phe		
		515					520					525					
cag	gcc	ggc	gag	ctg	aag	tgg	ggc	acc	gac	gag	gag	aag	ttc	atc	acc	1632	
Gln	Ala	Gly	Glu	Leu	Lys	Trp	Gly	Thr	Asp	Glu	Glu	Lys	Phe	Ile	Thr		
	530					535					540						
atc	ctg	ggc	acc	cgc	tcc	gtg	tcc	cac	ctg	cgc	cgc	gtg	ttc	gac	aag	1680	
Ile	Leu	Gly	Thr	Arg	Ser	Val	Ser	His	Leu	Arg	Arg	Val	Phe	Asp	Lys		
545					550					555					560		
tac	atg	acc	atc	tcc	ggc	ttc	cag	atc	gag	gag	acc	atc	gac	cgc	gag	1728	
Tyr	Met	Thr	Ile	Ser	Gly	Phe	Gln	Ile	Glu	Glu	Thr	Ile	Asp	Arg	Glu		
				565					570					575			
acc	tcc	ggc	aac	ctg	gag	aac	ctg	ctg	ctg	gcc	gtg	gtg	aag	tcc	atc	1776	
Thr	Ser	Gly	Asn	Leu	Glu	Asn	Leu	Leu	Leu	Ala	Val	Val	Lys	Ser	Ile		
			580					585					590				
cgc	tcc	atc	ccc	gcc	tac	ctg	gcc	gag	acc	ctg	tac	tac	gcc	atg	aag	1824	
Arg	Ser	Ile	Pro	Ala	Tyr	Leu	Ala	Glu	Thr	Leu	Tyr	Tyr	Ala	Met	Lys		

595	600	605	
ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc			1872
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg			
610	615	620	
tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc			1920
Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe			
625	630	635	640
gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac			1968
Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr			
	645	650	655
aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac taa taa taa			2016
Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp			
	660	665	

<210> 6
 <211> 669
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> The 'Xaa' at location 15 stands for Ser.

<220>
 <221> misc_feature
 <222> (334)..(334)
 <223> The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
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 <222> (351)..(351)
 <223> The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
 <223> primer

<400> 6

Met	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Leu	Ala	Ala	Ala	Asn	Xaa	Ala
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			20					25					30		

Ala	Glu	Val	Leu	Arg	Lys	Ala	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
50 55 60

Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
65 70 75 80

Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
85 90 95

Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
100 105 110

Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
115 120 125

Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
130 135 140

Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr
145 150 155 160

Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp
165 170 175

Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe
180 185 190

Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr
195 200 205

Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys
210 215 220

Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu
225 230 235 240

Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile
245 250 255

Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys
260 265 270

Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
 275 280 285

Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
 290 295 300

Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr
 305 310 315 320

Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser
 325 330 335

Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala
 340 345 350

Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
 355 360 365

Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
 370 375 380

Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
 385 390 395 400

Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
 405 410 415

Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
 420 425 430

Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
 435 440 445

Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
 450 455 460

Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
 465 470 475 480

Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr
 485 490 495

Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp
500 505 510

Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe
515 520 525

Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr
530 535 540

Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys
545 550 555 560

Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu
565 570 575

Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile
580 585 590

Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys
595 600 605

Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
610 615 620

Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
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